

EXHIBIT A

Alignment of amino acid sequences of glutaminases

		1	50
gls (2247)	(1)	MVAFESLWPNLSCTRVYSAKEIISLDSILMPPEYLHEILDDVRDITS	
GLSA_CORGL	(1)	-----LILMPPEYLHEILDDVRDITS	
GLSA_COREF	(1)	-----MTTHPLMPPEYFEEILSVRSVS	
GLSA1_BRAJA	(1)	-----TTPPASWTRSKPPLRLDTCLNFSATIS	
GLSA2_BRAJA	(1)	-----MDTQPIRLPSAGATRSGYPTRPPLRRLTICHELFRGSS	
GLSA_ANASP	(1)	-----SDQANQGDLEIRPSPLKVINLHISKYSLKE	
Consensus	(1)	MS SA MLTMPIEYL EILDDVRSDTS	
		51	100
gls (2247)	(51)	GELADYIPELKSADPNPLAVALCTVNGHYSAGDDDEFTIQSISKPFAY	
GLSA_CORGL	(23)	GELADYIPELKSADPNPLAVALCTVNGHYSAGDDDEFTIQSISKPFAY	
GLSA_COREF	(27)	GEVADYIPELKSADPNPLAVALCTVDGHIYGAGDDDEFTIQSISKPFAY	
GLSA1_BRAJA	(33)	GAVADYIPELGNADPAYFGISLATLDGHIYEVGDSRPFTIQSISKPFV	
GLSA2_BRAJA	(43)	GELADYIPELKRANPDHFGIALVTLDGHIYEVGDSAPFTIQSISKAFV	
GLSA_ANASP	(34)	GTIVANYIPELAKVNPDLFSISIVTVDGQVYQVDYQQLFTIQSISKVFAY	
Consensus	(51)	GELADYIPELKADPNPLATALCTVDGHIYVGDDDEFTIQSISKPFAY	
		101	150
gls (2247)	(101)	ALALQECGFDEVSAVALEPSGEAFNEISLDG-ENRPMNPMINAGATAIN	
GLSA_CORGL	(73)	ALALQECGFDEVSAVALEPSGEAFNEISLDG-ENRPMNPMINAGATAIN	
GLSA_COREF	(77)	ALALQECGPEKVFATVGLPEPSGEAFNEISLDGSTNRPMNPMINAGATAIN	
GLSA1_BRAJA	(83)	ALALDLLGAGRVESATIGVEPSGDPFNSRLNSDN-HPFNPMVNAGATACT	
GLSA2_BRAJA	(93)	ALALETVGGERVSATIGVEPSGEAFNSRLINDN-RPFNPMVNAGATAACS	
GLSA_ANASP	(84)	GLALEDHGRDYVLTTRVGVEPGEAFNAIILDEQSKRPYNPMINAGATAATT	
Consensus	(101)	ALALQEGDRVSASVGLPEPSGEAFNEISLDGNRPMNPMINAGATAIN	
		151	200
gls (2247)	(150)	QLINGSDSIVEDRVEKIRHYFSELAGRELIDRVLAESLAGADRNLSTIA	
GLSA_CORGL	(122)	QLINGSDSIVEDRVEKIRHYFSELAGRELIDRVLAESLAGADRNLSTIA	
GLSA_COREF	(127)	QLINGSSESVEDRVEKIRSYFSELAGRELNIDRQLSETELEGADRNLSTIA	
GLSA1_BRAJA	(132)	GLIYDSKG--AAFEQIRLALSRFAGRLAIDEAVSSESQTGDRNRAIG	
GLSA2_BRAJA	(142)	GLIYEVGG--KGAFERVRSKLSEFAGRELGVDEAVHASETATGNRNRATA	
GLSA_ANASP	(134)	SLIKGAG--TIRNRVLEMERRYIGHYFVQISVFTSERSTIGHNRNAMA	
Consensus	(151)	QLINGSDSIVEDRVEKIRYFSELAGRELIDRALAESLATADRNRATA	
		201	250
gls (2247)	(200)	HMLRNYGVIEDDAHDAVLSYTLQCAIKVTTRDLAVMTATLAAGGTHPITG	
GLSA_CORGL	(172)	HMLRNYGVIEDDAHDAVLSYTLQCAIKVTTRDLAVMTATLAAGGTHPITG	
GLSA_COREF	(177)	HMLRNYGVIEDDAHDAVLSYTLQCSVKVTARDLAVMTATLAAGGTQPTG	
GLSA1_BRAJA	(180)	YLLKTNVLSDNVAAVLVYFROCAVLTARDLAVMAATLANRGINPYTG	
GLSA2_BRAJA	(190)	YLLRNYAVLPDLDVAVLVYFROCAVLTARDLAVMAATLANRGINPYTG	
GLSA_ANASP	(182)	HLLNFGMTDRNIEEALDLYFQCCAMYNCHDLAVMAATLANRGVNPITG	
Consensus	(201)	HLLRNYGVIEDDAHDALLSYTLQCAIKVTARDLAVMTATLANRGINPYTG	
		251	300
gls (2247)	(250)	KKLDARVRLTSLVMASAGMYDEAGQWLSTVGIPAKSGVAGGIGILPG	
GLSA_CORGL	(222)	KKLDARVRLTSLVMASAGMYDEAGQWLSTVGIPAKSGVAGGIGILPG	
GLSA_COREF	(227)	EKLVDARVARLVLSLTMASAGMYDEAGQWLATVGIPAKSGVSGGLVGVLPG	
GLSA1_BRAJA	(230)	EDVMSAYASRTLSVMTSSGMYDYAGEVYRIGIPAKSGVGGGLAALPA	
GLSA2_BRAJA	(240)	ADVITPHIVARTLSVMTSSGMYDYAGEVYRIGIPAKSGVGGGIVAAALPS	
GLSA_ANASP	(232)	ECANNSRYIKDTLSVMTTCGMYNFAGEVAYKVGIPAKSGVCGGIMAVVPN	
Consensus	(251)	EQLLDARVIRLTSLVMASAGMYDEAGQWLYTVGIPAKSGVAGGIIATLPG	
		301	350
gls (2247)	(300)	QLGIATFSPRLNPKGNSVRGVKIFKALSDDMGLHLMSTEQVSGHAVRSIT	
GLSA_CORGL	(272)	QLGIATFSPRLNPKGNSVRGVKIFKALSDDMGLHLMSTEQVSGHAVRSIT	
GLSA_COREF	(277)	QLGIATFSPRLNSQGNPVRGVEIFKALSDDMGLHLMSEELTQHAVRAIE	
GLSA1_BRAJA	(280)	RLGLGSYSPKLDKHGNSVRGKYCEALSSHYDLHMLNRSDDRNAVITADY	
GLSA2_BRAJA	(290)	QLGIGTFSPRLDNHNSVRGLKYCEALSARFDLHMLNRNADVRTSYMADY	
GLSA_ANASP	(282)	LIGAVFSPPLDIRGNSVRGVKICEELSQQLGLHLEFCMKVNGGEWGVGN	
Consensus	(301)	QLGIATFSPRLNKGNSVRGVKIFKALSDDMGLHLMSEVS HAVRAI	
		351	400
gls (2247)	(350)	RG-----DTTFIQMGAMNFSASESELHAIVEH	
GLSA_CORGL	(322)	RG-----DTTFIQMGAMNFSASESELHAIVEH	
GLSA_COREF	(327)	ERG-----DTTIIQMGAMNFSASENELFTYD	
GLSA1_BRAJA	(330)	DIIGKSPSRVRRAQEREILAAHEQVRIITELVGTSLSAVYVSRRAGR	

GLSA2_BRAJA	(340)	IVYGISSRRSRQPHEQQILDERHSDIR ELVGA NFGTI YVTRR TSE
GLSA_ANASP	(332)	CEC-----
Consensus	(351)	DDG-----DTTIQLQGAMNFSASE FL I EH
		401-----450
gls (2247)	(379)	NFEGTEVVLDTLTVLSFHPVAIRM KEGLKRIRDAGFEVFLDPDDVLPD
GLSA_CORGL	(351)	NFEGTEVVLDTLTVLSFHPVAIRM KEGLKRIRDAGFEVFLDPDDVLPD
GLSA_COREF	(356)	DETGEKVVLDSRVPMFRPIGRRLVKEGLRIRDNGEKVALYDPEDILPD
GLSA1_BRAJA	(380)	P-RPQFVFDLHRVTSTTRAGARLVAEAFEEAALNVTVVSGVRRASKE
GLSA2_BRAJA	(390)	PPNPLIDFRRVPDITAAGAEIGETITAGNANVTTIISGLASAV
GLSA_ANASP	(335)	-----
Consensus	(401)	F G VVLDLTV SF PVG RLIEGLKRIRDAGF V I DPDDVLPD
		451-----500
gls (2247)	(429)	FMSDGTICKERV-----
GLSA_CORGL	(401)	FMSDGTICKERV-----
GLSA_COREF	(406)	FDFSDGTKSPQVDDPEEL-----
GLSA1_BRAJA	(429)	VNTLREWTAELINVRDFYLLDTAIEWAEDQIVYRYGGSIDFHETTELAEQ
GLSA2_BRAJA	(440)	AAIAARTGDPRLRRFALLDDAIEWAEDQVYRFGGFTDVKESVHLGEQ
GLSA_ANASP	(335)	-----
Consensus	(451)	F FSDGT R-----
		501-----550
gls (2247)	(442)	-----
GLSA_CORGL	(414)	-----
GLSA_COREF	(424)	-----
GLSA1_BRAJA	(479)	PLLEGLSADELAELGAICTIRTYQSGAKILTTGDPADALFFLRSGAVHVT
GLSA2_BRAJA	(490)	ALLAELDTDEIAAIVKLSTTRHYTAGQRVIAAGAPANSLFFLQSGMVSVK
GLSA_ANASP	(335)	-----
Consensus	(501)	-----
		551-----600
gls (2247)	(442)	-----
GLSA_CORGL	(414)	-----
GLSA_COREF	(424)	-----
GLSA1_BRAJA	(529)	LPDGVRLATLTAGMAFGEMALLEQTRSADVFADMAATAFEAPLKDFERFR
GLSA2_BRAJA	(540)	LRSGVRLASLPGMEFGEMAILERTRSADVFADTPVACLELPLDSFADYR
GLSA_ANASP	(335)	-----
Consensus	(551)	-----
		601-----635
gls (2247)	(442)	-----
GLSA_CORGL	(414)	-----
GLSA_COREF	(424)	-----
GLSA1_BRAJA	(579)	EQHPRASERIMRNLAQLLADRLIVANAKVDILTST
GLSA2_BRAJA	(590)	RLHPETALKIMRNLAAILARRLVAANAKVDLLSAY
GLSA_ANASP	(335)	-----
Consensus	(601)	-----

GLSA_CORGL : Q8NMT3; *Corynebacterium glutamicum*
 GLSA_COREF : Q8FMX4; *Corynebacterium efficiens*.
 GLSA1_BRAJA : Q89NA7; *Bradyrhizobium japonicum*,
 GLSA2_BRAJA : Q89KV2; *Bradyrhizobium japonicum*
 GLSA_ANASP : Q8YSZ5; *Anabaena* sp. (strain PCC 7120)